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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/669,781	09/24/2003	Juha Apajalahti	79428	6390
22242	7590	10/25/2006	EXAMINER	
FITCH EVEN TABIN AND FLANNERY 120 SOUTH LA SALLE STREET SUITE 1600 CHICAGO, IL 60603-3406			FRONDA, CHRISTIAN L	
			ART UNIT	PAPER NUMBER
			1652	

DATE MAILED: 10/25/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)
	10/669,781	APAJALAHTI ET AL.
	Examiner Christian L. Fronda	Art Unit 1652

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) Responsive to communication(s) filed on 28 August 2006.
 2a) This action is FINAL. 2b) This action is non-final.
 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4) Claim(s) 1-12 is/are pending in the application.
 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
 5) Claim(s) _____ is/are allowed.
 6) Claim(s) 1-12 is/are rejected.
 7) Claim(s) _____ is/are objected to.
 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9) The specification is objected to by the Examiner.
 10) The drawing(s) filed on 24 October 2003 is/are: a) accepted or b) objected to by the Examiner.
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. 10/251,503.
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) Notice of References Cited (PTO-892)
 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)
 3) Information Disclosure Statement(s) (PTO/SB/08)
 Paper No(s)/Mail Date 08/23/06.

4) Interview Summary (PTO-413)
 Paper No(s)/Mail Date. _____.
 5) Notice of Informal Patent Application
 6) Other: RSL Error Report.

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DETAILED ACTION

1. Claims 1-12 are pending and under consideration in this Office Action.
2. The rejection of claim 10 under 35 U.S.C. 112, second paragraph, as being indefinite has been withdrawn in view of applicants' arguments and amendment to the claim filed 08/28/2006.

NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

3. This application fails to comply with the requirements of 37 CFR §§ 1.821 through 1.825 for the reason(s) set forth: certain errors were detected by the STIC Biotechnology Systems Branch. Please see the attached paper **RAW SEQUENCE LISTING ERROR REPORT**.

Claim Rejections - 35 U.S.C. § 112, 1st Paragraph

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.
5. Claims 1-12 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid of SEQ ID NO: 1, an isolated host cell transformed with a nucleic acid of SEQ ID NO: 1, and a method for identifying a nucleic acid molecule which encodes a phytase using SEQ ID NO: 1, and a method for the production of the nucleic acid sequence of SEQ ID NO: 1 using the specific PCR primers listed on page 25 of the specification; does not reasonably provide enablement for any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions and any method for the production of any nucleic acid which encodes a phytase using any two or more PCR primers which hybridize to SEQ ID NO: 1 or to any complement of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Applicants' arguments filed 08/28/2006 have been fully considered but are not

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persuasive. The examiner respectfully disagrees with applicants' position that one of ordinary skill in the art would understand what conditions are needed to provide high stringency for Southern blotting.

The nature and breadth of the claims encompass any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions. Applicants have not sufficiently defined the conditions under which the hybridizations are to take place. Nucleic acid hybridization assays are extremely sensitive to the conditions in which they are performed. The buffer composition, pH, temperature, length of time, salt concentrations, quality and source of template nucleic acid, are all variables which determine the reproducibility of a given hybridization experiment.

Given the unpredictability of the art and the nature of hybridization experiments in general, it is not sufficient to merely cite hybridization without a clear and explicit recitation of the conditions associated with the hybridization. For example, the definition of stringency as it pertains to hybridization conditions is subject to interpretation and is different from laboratory to laboratory. Therefore, without a clear and explicit recitation of the conditions which were actually used by Applicants in isolating the claimed polynucleotides which hybridize to the disclosed sequences, the skilled artisan would not be able to practice the claimed invention and would not be reasonably apprised of the metes and bounds of the claimed invention. Without such guidance, the experimentation left to those skilled in the art is undue. Including in the claims the exact nature of the hybridization conditions, such as salt concentration and temperature, would aid in overcoming this portion of the rejection.

Conclusion

6. No claim is allowed.

7. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

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8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Christian L Fronda whose telephone number is (571)272-0929. The examiner can normally be reached Monday-Friday between 9:00AM - 5:00PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura N Achutamurthy can be reached on (571)272-0928. The fax phone number for the organization where this application or proceeding is assigned is (571)273-8300.

9. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

CLF


TEKCHAND SAIDHA
PRIMARY EXAMINER

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/669,781A
Source: 1FW16
Date Processed by STIC: 8/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

3 <110> APPLICANT: Finnfeeds International, Ltd.
 5 <120> TITLE OF INVENTION: Phytase from *Bacillus subtilis*, gene encoding said phytase,
 6 method for its production and use
 8 <130> FILE REFERENCE: 79428
 10 <140> CURRENT APPLICATION NUMBER: 10/669,781A see pp 1-10
 11 <141> CURRENT FILING DATE: 2003-09-24
 13 <160> NUMBER OF SEQ ID NOS: 36
 15 <170> SOFTWARE: PatentIn version 3.3

ERRORED SEQUENCES

E--> 17 <210> SEQ ID NO: ~~SEQ ID NO:1~~ do not insert alphabetical headings. The CRF Software will insert them for clarity.
 18 <211> LENGTH: 1290
 19 <212> TYPE: DNA
 20 <213> ORGANISM: *Bacillus subtilis*; Strain: B13
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (91)..(1239)
 27 <400> SEQUENCE: 1
 28 cacatttgac aattttcaca aaaaacttaac actgacaatc atgtatataat gttacaattg 60
 30 aagtgcacgt tcataaaaagg aggaagtaaa atg aat cat tca aaa aca ctt ttg 114
 31 Met Asn His Ser Lys Thr Leu Leu
 32 1 5
 34 tta acc gcg gcg gcc gga ctg atg ctc aca tgc ggt gcg gtg tct tcc 162
 35 Leu Thr Ala Ala Gly Leu Met Leu Thr Cys Gly Ala Val Ser Ser
 36 10 15 20
 38 cag gca aag cat aag ctg tcc gat cct tat cat ttt acc gtg aat gca 210
 39 Gln Ala Lys His Lys Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala
 40 25 30 35 40
 42 gcg gcg gaa acg gaa ccg gtt gat acg gcc ggt gac gcg gct gat gat 258
 43 Ala Ala Glu Thr Glu Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp
 44 45 50 55
 46 cct gcg att tgg ctg gac ccc aag act cct cag aac agc aaa ttg att 306
 47 Pro Ala Ile Trp Leu Asp Pro Lys Thr Pro Gln Asn Ser Lys Leu Ile
 48 60 65 70
 50 acg acc aat aaa aaa tca ggt tta gtc gtt tac agc ctt gat ggt aag 354
 51 Thr Thr Asn Lys Lys Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys
 52 75 80 85
 54 atg ctt cat tcc tat aat acc ggg aag ctg aac aat gtc gat atc cgt 402
 55 Met Leu His Ser Tyr Asn Thr Gly Lys Leu Asn Asn Val Asp Ile Arg
 56 90 95 100
 58 tat gat ttt ccg ttg aac ggc aaa aaa gtc gat atc gcg gca tcc 450

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:33

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62	aat	cgg	tct	gaa	gga	aaa	aat	acc	att	gag	att	tac	gct	att	gat	gga	498
63	Asn	Arg	Ser	Glu	Gly	Lys	Asn	Thr	Ile	Glu	Ile	Tyr	Ala	Ile	Asp	Gly	
64						125				130				135			
66	aaa	aac	ggc	aca	tta	caa	agc	atg	aca	gat	cca	gac	cat	ccg	att	gca	546
67	Lys	Asn	Gly	Thr	Leu	Gln	Ser	Met	Thr	Asp	Pro	Asp	His	Pro	Ile	Ala	
68						140				145				150			
70	aca	gca	att	aat	gag	gta	tac	ggt	ttt	acc	tta	tac	cac	agt	caa	aaa	594
71	Thr	Ala	Ile	Asn	Glu	Val	Tyr	Gly	Phe	Thr	Leu	Tyr	His	Ser	Gln	Lys	
72						155				160				165			
74	aca	gga	aaa	tat	tac	gcg	atg	gtg	aca	gga	aaa	gag	ggt	gaa	ttt	gaa	642
75	Thr	Gly	Lys	Tyr	Tyr	Ala	Met	Val	Thr	Gly	Lys	Glu	Gly	Glu	Phe	Glu	
76						170				175				180			
78	caa	taa	gaa	tta	aag	gca	gac	aaa	aat	gga	taa	tcc	ggc	aaa	aag		690
79	Gln	Tyr	Glu	Leu	Lys	Ala	Asp	Lys	Asn	Gly	Tyr	Ile	Ser	Gly	Lys		
80	185					190				195				200			
82	gta	cg	g	ttt	aaa	atg	aat	tcc	cag	acg	gaa	ggg	atg	gca	gca	gac	738
83	Val	Arg	Ala	Phe	Lys	Met	Asn	Ser	Gln	Thr	Glu	Gly	Met	Ala	Ala	Asp	
84						205				210				215			
86	gat	gaa	taa	gca	ggc	agg	ctt	tat	atc	gca	gaa	gaa	gat	gag	gcc	att	786
87	Asp	Glu	Tyr	Gly	Arg	Leu	Tyr	Ile	Ala	Glu	Glu	Asp	Glu	Ala	Ile	Trp	
88						220				225				230			
90	aag	ttc	agc	gcc	gag	ccg	gac	ggc	agt	aac	gga	acg	gtt	atc	gac		834
91	Lys	Phe	Ser	Ala	Glu	Pro	Asp	Gly	Gly	Ser	Asn	Gly	Thr	Val	Ile	Asp	
92						235				240				245			
94	cgt	gcc	gac	ggc	agg	cat	tta	act	cgt	gat	att	gaa	gga	ttg	acg	att	882
95	Arg	Ala	Asp	Gly	Arg	His	Leu	Thr	Arg	Asp	Ile	Glu	Gly	Leu	Thr	Ile	
96						250				255				260			
98	taa	taa	gct	gct	gac	ggg	aaa	ggc	tat	ctg	atg	gca	tca	agc	cag	gga	930
99	Tyr	Tyr	Ala	Ala	Asp	Gly	Lys	Gly	Tyr	Leu	Met	Ala	Ser	Ser	Gln	Gly	
100	265					270				275				280			
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103	Asn	Ser	Ser	Tyr	Ala	Ile	Tyr	Asp	Arg	Gln	Gly	Lys	Asn	Lys	Tyr	Val	
104						285				290				295			
106	gca	gat	ttt	cgc	ata	aca	gac	ggt	cct	gaa	aca	gac	ggg	aca	agc	gat	1026
107	Ala	Asp	Phe	Arg	Ile	Thr	Asp	Gly	Pro	Glu	Thr	Asp	Gly	Thr	Ser	Asp	
108						300				305				310			
110	aca	gac	gga	att	gac	gtt	ctg	ggt	ttc	gga	ctg	ggg	cct	gaa	tat	ccg	1074
111	Thr	Asp	Gly	Ile	Asp	Val	Leu	Gly	Phe	Gly	Leu	Gly	Pro	Glu	Tyr	Pro	
112						315				320				325			
114	ttc	ggt	att	ttt	gtc	gca	cag	gac	ggt	gaa	aat	ata	gat	cac	ggc	caa	1122
115	Phe	Gly	Ile	Phe	Val	Ala	Gln	Asp	Gly	Glu	Asn	Ile	Asp	His	Gly	Gln	
116						330				335				340			
118	aag	gcc	aat	caa	aat	ttt	aaa	atc	gtg	cca	tgg	gaa	aga	att	gct	gat	1170
119	Lys	Ala	Asn	Gln	Asn	Phe	Lys	Ile	Val	Pro	Trp	Glu	Arg	Ile	Ala	Asp	
120	345					350				355				360			
122	caa	atc	ggt	ttc	cgc	ccg	ctg	gca	aat	gaa	cag	gtt	gac	ccg	aga	aaa	1218
123	Gln	Ile	Gly	Phe	Arg	Pro	Leu	Ala	Asn	Glu	Gln	Val	Asp	Pro	Arg	Lys	

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006
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124 365 370 375 1269
 126 ctg acc gac aga agc gga aaa taaacatgca aaaaggcagct tataacaagct
 127 Leu Thr Asp Arg Ser Gly Lys
 128 380
 130 gctttttgca tgtgaagaac g 1290
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 134 <211> LENGTH: 383
 135 <212> TYPE: PRT
 136 <213> ORGANISM: *Bacillus subtilis*; Strain: B13
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 144 Leu Thr Cys Gly Ala Val Ser Ser Gln Ala Lys His Lys Leu Ser Asp
 145 20 25 30
 148 Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu Pro Val Asp
 149 35 40 45
 152 Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Trp Leu Asp Pro Lys
 153 50 55 60
 156 Thr Pro Gln Asn Ser Lys Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu
 157 65 70 75 80
 160 Val Val Tyr Ser Leu Asp Gly Lys Met Leu His Ser Tyr Asn Thr Gly
 161 85 90 95
 164 Lys Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
 165 100 105 110
 168 Lys Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys Asn Thr
 169 115 120 125
 172 Ile Glu Ile Tyr Ala Ile Asp Gly Lys Asn Gly Thr Leu Gln Ser Met
 173 130 135 140
 176 Thr Asp Pro Asp His Pro Ile Ala Thr Ala Ile Asn Glu Val Tyr Gly
 177 145 150 155 160
 180 Phe Thr Leu Tyr His Ser Gln Lys Thr Gly Lys Tyr Tyr Ala Met Val
 181 165 170 175
 184 Thr Gly Lys Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys Ala Asp Lys
 185 180 185 190
 188 Asn Gly Tyr Ile Ser Gly Lys Lys Val Arg Ala Phe Lys Met Asn Ser
 189 195 200 205
 192 Gln Thr Glu Gly Met Ala Ala Asp Asp Glu Tyr Gly Arg Leu Tyr Ile
 193 210 215 220
 196 Ala Glu Glu Asp Glu Ala Ile Trp Lys Phe Ser Ala Glu Pro Asp Gly
 197 225 230 235 240
 200 Gly Ser Asn Gly Thr Val Ile Asp Arg Ala Asp Gly Arg His Leu Thr
 201 245 250 255
 204 Arg Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Ala Ala Asp Gly Lys Gly
 205 260 265 270
 208 Tyr Leu Met Ala Ser Ser Gln Gly Asn Ser Ser Tyr Ala Ile Tyr Asp
 209 275 280 285
 212 Arg Gln Gly Lys Asn Lys Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly
 213 290 295 300
 216 Pro Glu Thr Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Leu Gly

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/669,781ADATE: 08/30/2006
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217 305 310 315 320
220 Phe Gly Leu Gly Pro Glu Tyr Pro Phe Gly Ile Phe Val Ala Gln Asp
221 325 330 335
224 Gly Glu Asn Ile Asp His Gly Gln Lys Ala Asn Gln Asn Phe Lys Ile
225 340 345 350
228 Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala
229 355 360 365
232 Asn Glu Gln Val Asp Pro Arg Lys Leu Thr Asp Arg Ser Gly Lys
233 370 375 380

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237 <211> LENGTH: 25
238 <212> TYPE: PRT
239 <213> ORGANISM: Bacillus subtilis
W--> 241 <400> SEQUENCE: 3
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244 1 5 10 15
247 Pro Val Asp Thr Ala Gly Asp Ala Ala
248 20 25

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253 <212> TYPE: PRT
254 <213> ORGANISM: Bacillus subtilis
W--> 256 <400> SEQUENCE: 4
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259 1 5 10 15
262 Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Leu Asp
263 20 25 30

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267 <211> LENGTH: 8
268 <212> TYPE: PRT
269 <213> ORGANISM: Bacillus subtilis
W--> 271 <400> SEQUENCE: 5
273 Tyr Tyr Ala Met Val Thr Gly Lys
274 1 5

E--> 277 <210> SEQ ID NO: ~~SEQ_ID_NO+6~~
278 <211> LENGTH: 10
279 <212> TYPE: PRT
280 <213> ORGANISM: Bacillus subtilis
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284 Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys
285 1 5 10

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291 <213> ORGANISM: Bacillus subtilis
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295 Met Leu His Ser Tyr Asn Thr Gly Lys
296 1 5

E--> 299 <210> SEQ ID NO: ~~SEQ_ID_NO+8~~

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006
TIME: 10:14:34

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Output Set: N:\CRF4\08302006\J669781A.raw

300 <211> LENGTH: 6
301 <212> TYPE: PRT
302 <213> ORGANISM: Bacillus subtilis
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306 Ile Val Pro Trp Glu Arg
307 1 5
E--> 310 <210> SEQ ID NO: ~~SEQ_ID_NO:9~~
311 <211> LENGTH: 25
312 <212> TYPE: PRT
313 <213> ORGANISM: Bacillus subtilis
E-> 315 <400> SEQUENCE: 9
317 Ile Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu
318 1 5 10 15
321 Ala Asn Glu Gln Val Asp Pro Arg Lys
322 20 25
E--> 325 <210> SEQ ID NO: ~~SEQ_ID_NO:10~~
326 <211> LENGTH: 30
327 <212> TYPE: PRT
328 <213> ORGANISM: Bacillus subtilis
E-> 330 <400> SEQUENCE: 10
332 Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala Thr
333 1 5 10 15
336 Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Trp His Ser Gln
337 20 25 30
E--> 340 <210> SEQ ID NO: ~~SEQ_ID_NO:11~~
341 <211> LENGTH: 23
342 <212> TYPE: PRT
343 <213> ORGANISM: Bacillus subtilis
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347 Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr
348 1 5 10 15
351 Ser Asp Asp Asp Gly Ile Ile
352 20
E--> 355 <210> SEQ ID NO: ~~SEQ_ID_NO:12~~
356 <211> LENGTH: 7
357 <212> TYPE: PRT
358 <213> ORGANISM: Bacillus subtilis
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362 Leu Thr Asp Arg Ser Gly Lys
363 1 5
E--> 366 <210> SEQ ID NO: ~~SEQ_ID_NO:13~~
367 <211> LENGTH: 13
368 <212> TYPE: PRT
369 <213> ORGANISM: Bacillus subtilis
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373 Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys
374 1 5 10
E--> 377 <210> SEQ ID NO: ~~SEQ_ID_NO:14~~
378 <211> LENGTH: 19

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

379 <212> TYPE: PRT
380 <213> ORGANISM: Bacillus subtilis
E--> 382 <400> SEQUENCE: 14
384 Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp
385 1 5 10 15
388 Pro Arg Lys
E--> 392 <210> SEQ ID NO: SEQ_ID_NO+15
393 <211> LENGTH: 6
394 <212> TYPE: PRT
395 <213> ORGANISM: Bacillus subtilis
E--> 397 <400> SEQUENCE: 15
399 Ala Asn Gln Asn Phe Lys
400 1 5
E--> 403 <210> SEQ ID NO: SEQ_ID_NO+16
404 <211> LENGTH: 5
405 <212> TYPE: PRT
406 <213> ORGANISM: Bacillus subtilis
E--> 408 <400> SEQUENCE: 16
410 Val Arg Ala Phe Lys
411 1 5
E--> 414 <210> SEQ ID NO: SEQ_ID_NO+17
415 <211> LENGTH: 11
416 <212> TYPE: PRT
417 <213> ORGANISM: Bacillus subtilis
E--> 419 <400> SEQUENCE: 17
421 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro
422 1 5 10
E--> 425 <210> SEQ ID NO: SEQ_ID_NO+18
426 <211> LENGTH: 15
427 <212> TYPE: PRT
428 <213> ORGANISM: Bacillus subtilis
E--> 430 <400> SEQUENCE: 18
432 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
433 1 5 10 15
E--> 436 <210> SEQ ID NO: SEQ_ID_NO+19
437 <211> LENGTH: 11
438 <212> TYPE: PRT
439 <213> ORGANISM: Bacillus subtilis
E--> 441 <400> SEQUENCE: 19
443 Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly Lys
444 1 5 10
E--> 447 <210> SEQ ID NO: SEQ_ID_NO+20
448 <211> LENGTH: 11
449 <212> TYPE: PRT
450 <213> ORGANISM: Bacillus subtilis
E--> 452 <400> SEQUENCE: 20
454 Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys
455 1 5 10
E--> 458 <210> SEQ ID NO: SEQ_ID_NO+21

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/669,781A

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Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

459 <211> LENGTH: 22
460 <212> TYPE: PRT
461 <213> ORGANISM: *Bacillus subtilis*
E-> 463 <400> SEQUENCE: 21
465 Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp Arg
466 1 5 10 15
469 Ala Asp Gly Arg His Leu
470 20
E--> 473 <210> SEQ ID NO: ~~SEQ-ID NO:22~~
474 <211> LENGTH: 23
475 <212> TYPE: DNA
476 <213> ORGANISM: Artificial
478 <220> FEATURE:
479 <223> OTHER INFORMATION: Synthesized
482 <220> FEATURE:
483 <221> NAME/KEY: modified_base
484 <222> LOCATION: (1)..(23)
485 <223> OTHER INFORMATION: All Ns represents inosine
E-> 487 <400> SEQUENCE: 22
W--> 488 tcngatccnt atcattttac ngt 23
E--> 491 <210> SEQ ID NO: ~~SEQ-ID NO:23~~
492 <211> LENGTH: 23
493 <212> TYPE: DNA
494 <213> ORGANISM: Artificial
496 <220> FEATURE:
497 <223> OTHER INFORMATION: Synthesized
500 <220> FEATURE:
501 <221> NAME/KEY: modified_base
502 <222> LOCATION: (1)..(23)
503 <223> OTHER INFORMATION: N represents inosine
E-> 506 <400> SEQUENCE: 23
507 agmggaaaaat catancyrat atc 23
E--> 510 <210> SEQ ID NO: ~~SEQ-ID NO:24~~
511 <211> LENGTH: 22
512 <212> TYPE: DNA
513 <213> ORGANISM: Artificial
515 <220> FEATURE:
516 <223> OTHER INFORMATION: Synthesized
518 <220> FEATURE:
519 <221> NAME/KEY: modified_base
520 <222> LOCATION: (1)..(22)
521 <223> OTHER INFORMATION: All N's represent inosine
E-> 523 <400> SEQUENCE: 24
524 cttcnganck rttnangcn gc 22
E--> 527 <210> SEQ ID NO: ~~SEQ-ID NO:25~~
528 <211> LENGTH: 20
529 <212> TYPE: DNA
530 <213> ORGANISM: Artificial
532 <220> FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/669,781A

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Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

533 <223> OTHER INFORMATION: Synthesized
 536 <220> FEATURE:
 537 <221> NAME/KEY: modified_base
 538 <222> LOCATION: (1)..(20)
 539 <223> OTHER INFORMATION: All N's represent inosine
 541 <400> SEQUENCE: 25
 542 tgatcngcra tnckttccca
 E--> 545 <210> SEQ ID NO: ~~SEQ-ID NO+26~~ 20
 546 <211> LENGTH: 20
 547 <212> TYPE: DNA
 548 <213> ORGANISM: Artificial
 550 <220> FEATURE:
 551 <223> OTHER INFORMATION: Synthesized
 553 <400> SEQUENCE: 26
 554 gcratmggat gatcmggatc
 E--> 557 <210> SEQ ID NO: ~~SEQ-ID NO+27~~ 20
 558 <211> LENGTH: 21
 559 <212> TYPE: DNA
 560 <213> ORGANISM: Artificial
 562 <220> FEATURE:
 563 <223> OTHER INFORMATION: Synthesized
 566 <220> FEATURE:
 567 <221> NAME/KEY: modified_base
 568 <222> LOCATION: (1)..(21)
 569 <223> OTHER INFORMATION: N represents inosine
 571 <400> SEQUENCE: 27
 572 ttcataytgt tcaaattcnc c
 E--> 575 <210> SEQ ID NO: ~~SEQ-ID NO+28~~ 21
 576 <211> LENGTH: 26
 577 <212> TYPE: DNA
 578 <213> ORGANISM: Artificial
 580 <220> FEATURE:
 581 <223> OTHER INFORMATION: Synthesized
 584 <220> FEATURE:
 585 <221> NAME/KEY: modified_base
 586 <222> LOCATION: (1)..(26)
 587 <223> OTHER INFORMATION: All N's represent inosine
 589 <400> SEQUENCE: 28
 590 ttnccngtrt tatangaatg narcat
 E--> 593 <210> SEQ ID NO: ~~SEQ-ID NO+29~~ 26
 594 <211> LENGTH: 20
 595 <212> TYPE: DNA
 596 <213> ORGANISM: Artificial
 598 <220> FEATURE:
 599 <223> OTHER INFORMATION: Synthesized
 602 <220> FEATURE:
 603 <221> NAME/KEY: modified_base
 604 <222> LOCATION: (1)..(20)
 605 <223> OTHER INFORMATION: N represents inosine

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/669,781A

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Input Set : F:\6031.79428 sequence.listing.ST25.txt
 Output Set: N:\CRF4\08302006\J669781A.raw

607 <400> SEQUENCE: 29
 608 ccatcratng catarattc 20
 E--> 611 <210> SEQ ID NO: ~~SEQ ID NO:30~~
 612 <211> LENGTH: 18
 613 <212> TYPE: DNA
 614 <213> ORGANISM: Artificial
 616 <220> FEATURE:
 617 <223> OTHER INFORMATION: Synthesized
 620 <220> FEATURE:
 621 <221> NAME/KEY: modified_base
 622 <222> LOCATION: (1)..(18)
 623 <223> OTHER INFORMATION: N represents inosine
 626 <400> SEQUENCE: 30 18
 627 tttaaarttgygrttngc
 E--> 630 <210> SEQ ID NO: ~~SEQ ID NO:31~~
 631 <211> LENGTH: 18
 632 <212> TYPE: DNA
 633 <213> ORGANISM: Artificial
 635 <220> FEATURE:
 636 <223> OTHER INFORMATION: Synthesized
 639 <220> FEATURE:
 640 <221> NAME/KEY: modified_base
 641 <222> LOCATION: (1)..(18)
 642 <223> OTHER INFORMATION: All N's represent inosine
 645 <400> SEQUENCE: 31
 646 tttnccngtn accatngc 18
 E--> 649 <210> SEQ ID NO: ~~SEQ ID NO:32~~
 650 <211> LENGTH: 38
 651 <212> TYPE: DNA
 652 <213> ORGANISM: Artificial
 654 <220> FEATURE:
 655 <223> OTHER INFORMATION: Synthesized
 658 <220> FEATURE:
 659 <221> NAME/KEY: misc_feature
 660 <222> LOCATION: (21)..(21)
 661 <223> OTHER INFORMATION: n is a, c, g, or t
 663 <400> SEQUENCE: 32 38
 664 gayccdtayc ayttaycdgt naaygcdgcd gcdgaaac
 E--> 667 <210> SEQ ID NO: ~~SEQ ID NO:33~~
 668 <211> LENGTH: 52
 669 <212> TYPE: DNA
 670 <213> ORGANISM: Artificial
 672 <220> FEATURE:
 673 <223> OTHER INFORMATION: Synthesized
 676 <220> FEATURE:
 677 <221> NAME/KEY: misc_feature
 678 <222> LOCATION: (7)..(14)
 679 <223> OTHER INFORMATION: Mfe I site
 681 <220> FEATURE:

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006
 TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt
 Output Set: N:\CRF4\08302006\J669781A.raw

682 <221> NAME/KEY: RBS
 683 <222> LOCATION: (14)..(19)
 685 <220> FEATURE:
 686 <221> NAME/KEY: CDS
 687 <222> LOCATION: (27)..(50)
 E-> 689 <400> SEQUENCE: 33
 690 gtttctcaat tgaaggagga atttaa atg ctg tcc gat cct tat cat ttt ac 52
 691 Met Leu Ser Asp Pro Tyr His Phe
 692 1 5
 E--> 695 <210> SEQ ID NO: ~~SEQ_ID_NO+34~~
 696 <211> LENGTH: 8
 697 <212> TYPE: PRT
 698 <213> ORGANISM: Artificial
 700 <220> FEATURE:
 701 <223> OTHER INFORMATION: Synthetic Construct
 E-> 703 <400> SEQUENCE: 34
 705 Met Leu Ser Asp Pro Tyr His Phe
 706 1 5
 E--> 709 <210> SEQ ID NO: ~~SEQ_ID_NO+35~~
 710 <211> LENGTH: 35
 711 <212> TYPE: DNA
 712 <213> ORGANISM: Artificial
 714 <220> FEATURE:
 715 <223> OTHER INFORMATION: Synthesized
 718 <220> FEATURE:
 719 <221> NAME/KEY: misc_feature
 720 <222> LOCATION: (6)..(11)
 721 <223> OTHER INFORMATION: Sal I site
 E-> 723 <400> SEQUENCE: 35
 724 aataaagtgcga cgtacgaccg gattccggct gtgct 35
 E--> 727 <210> SEQ ID NO: ~~SEQ_ID_NO+36~~
 728 <211> LENGTH: 34
 729 <212> TYPE: DNA
 730 <213> ORGANISM: Artificial
 732 <220> FEATURE:
 733 <223> OTHER INFORMATION: Synthesized
 736 <220> FEATURE:
 737 <221> NAME/KEY: misc_feature
 738 <222> LOCATION: (6)..(11)
 739 <223> OTHER INFORMATION: Bgl II site
 E-> 741 <400> SEQUENCE: 36
 742 aataaaagatc ttttccgct tctgtcggtc agtt 34

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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/669,781A

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TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:27 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:138 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:241 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:266 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:271 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
L:288 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:299 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:304 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
L:325 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
L:340 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
L:355 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:360 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
L:366 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:371 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
L:377 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
L:392 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:397 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
L:403 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
L:414 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:419 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
L:425 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:430 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
L:436 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:441 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:452 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
L:458 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:463 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
L:473 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:487 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:491 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:23
M:341 Repeated in SeqNo=0

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt
Output Set: N:\CRF4\08302006\J669781A.raw

L:510 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:523 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:24
L:527 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:541 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:25